FIG. 1

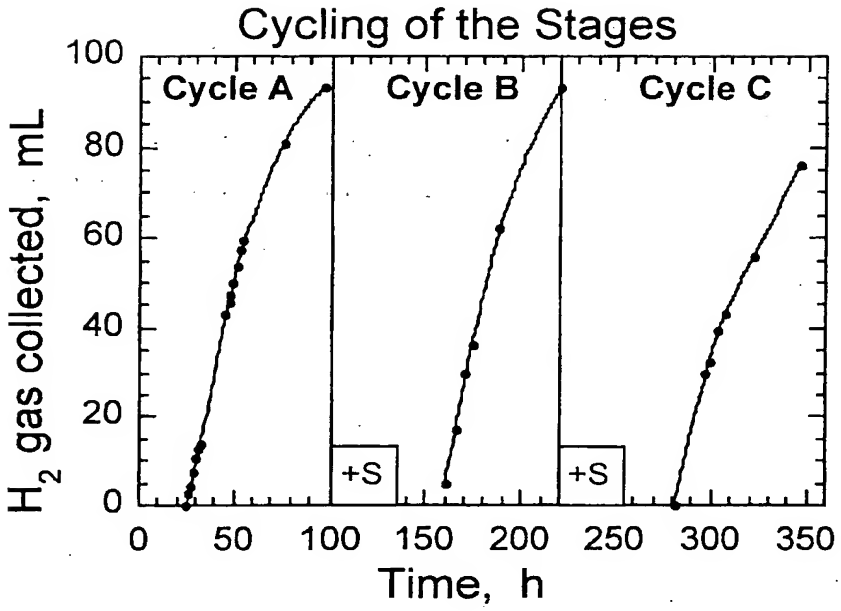

FIG. 2

Chlamydomonas reinhardtii chloroplast Sulfate Permease (*SulP*) gene structure

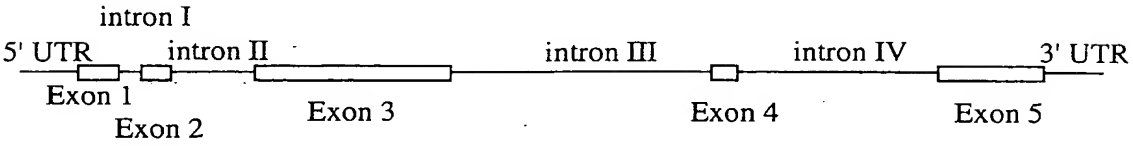

FIG. 3

reinhardtii chloroplast Sulfate Permease *(SulP)* amino acid sequence

MERVCSHQLASSRGRPCIAGVQRSPIRLGTSSVAHVQVSPAGLGRYQRQRLQVVASAAAA
AAFDPPGGVSAGFSQPQQQLPQQHPRQPQAVAEVAVAESVSAPASAAPSNDGSPTASMDG
GPSSGLSAVPAAATATDLFSAAARLRLPNLSPIITWTFMLSYMAFMLIMPITALLQKASL
VPLNVFIARATEPVAMHAYYVTFSCSLIAAAINCVFGFVLAWVLVRYNFAGKKILDAAVD
LPFALPTSVAGLTLATVYGDEFFIGQFLQAQGVQVVFTRLGVVIAMIFVSFPFVVRTMQP
VMQEIQKEMEEAAWSLGASQWRTFTDVVLPPLLPALLTGTALAFSRALGEFGSIVIVSSN
FAFKDLIAPVLIFQCLEQYDYVGATVIGTVLLLISLVMMLAVNQLQKLARK* (SEQ ID NO:1)

FIG. 4A

Coding sequence of CrcpSulP

5' UTR:173 bp, Exon1: 124 bp, intronI: 77 bp, Exon2: 78 bp,
intronII: 279 bp Exon3: 620 bp, intronIII: 834 bp,
Exon4: 87 bp, intronIV: 699 bp, Exon5: 327 bp, 3'UTR: 575 bp

Total length: 3873 bp

```
gcttagtacc taagcaaaaa taccaaagcc ttatcctgag ttgtcaacaa gaactccagc 60
ctgcgacgat gcaaagcctt tcttgagcgg gttgatggac tttgctttgt tatctgtcca 120
gtaagccacc agacactacc aagtagagta atccatttgt ataggtacag aatatggagc 180
gagtttgcag ccatcagctt gcctcgtcgc gagggaggcc atgcatcgct ggggtgcagc 240
ggtcgcccat ccgactaggg acttcaagcg ttgctcatgt gcaggtctct ccggcaggta 300
agcaccgcgc tcggcggcgt gtacacatgg ggccgtcagg ccaactgcgt ttgttggcta 360
tgcaaccgaa acaggccttg ggagatatca acggcaaaga ctgcaagtcg tggcgtctgc 420
agctgcggca gcggctttcg accctcctgg aggtgcgtgg cgtgagggct gcacgggtgc 480
gggttggcct ggaaaccaag cctcgccacg actacctgca acagcattgc ccgcatctcc 540
agcccctcac cctcgagtgc ctcccgaaga cctctatccc ctgcgcatca ttggttcggg 600
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gctccccgca ggtgtctccg ccgggttctc gcagccgcaa cagcagctgc cacaacagca 780
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ttctgcggcg ccctccaatg atggctcgcc cacggcctcc atggacggcg gccccagctc 900
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cggccagttc ctgcaggcgc agggcgtgca ggtgcgtgcg tatagcatag tggagtgtgg 1380
ttagcagctg ggggtccggc agtagttccc gccctagtga ggtcgaaact ataccagaag 1440
aagaggacga acatggggct atccagcaag ctcgtctagg gaaggaggag tttgggagaa 1500
cggtggggtg ggagggagag ggagggcgtt ggctgggagg gaagggtaag gcgggaggga 1560
gatggtagca cggggcgttg gggacgcaga aggatgacag gcggctgcag ggaagggatg 1620
gggaagcgga gctggggaca gtgcgaagag ccgggagaga ggggaagttt gagtcaggaa 1680
gaggggctag agaggggcat gcggactcct gctgggattt aggtgcgtgc tcattgagga 1740
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cccgcagttg gaggatgctc cacgcgcttc agcttgccat gtctggggtc tgggtctgga 2040
cgcaatcagc gtgtgagggt ccaactctat atggaattat ggataccttc caactaccag 2100
cacgtaggct gccggaacgc ggctgaagcg gctggcctgc cccctcatcc tctcgttccc 2160
```

FIG. 4B

ctgtttttgt cccctgtcca cccaggtggt gttcacgcgg ctgggtgtgg tgatcgccat 2220
gatcttcgtg tccttcccct tcgtggtgcg caccatgcag cccgtcatgc aggtgagagc 2280
gcccaggagg cggagccatg gcgggttggg gcgggttggg gcgggttggg gcggggcgcg 2340
gatggggcgg cttggggagt aatgtggggc ggatggggtg gcagcctggc agggtatggg 2400
agcgagagga tagcggggac aggggacagg gaagggaagg gaaggggaag gatgccctat 2460
gcgagcaaag ggggtatggg aaccggcggt tggggctggg agcgacggga gcagggaggg 2520
agtgcacgga acgggggcaa ggcggacagg gtgagggagg gtgcaggccg gactgggatg 2580
ggtcatgtgt cctggtcggg ggtgtagccg tgggaggcgg gcaggcagcg tgtgttctgg 2640
cacggtgttt tggcgaaaga taccacggca tggtatgggg ccagttgggc agggaagaac 2700
cgttggacac gacttcgttg acagatctag ttcattgcac ccgggtcgca ccaagggtgg 2760
cggcgagccc ggcccggcac gtccgagtac cccggagccg taacgccgca acccgccttg 2820
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gaggaggttg cagggtgagg caggagtggc aggtggtgga gggtgcaggg cggggtgttg 3420
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tgcaagctca ggcagtcgca tgcccgtacc ctgcttctgg tccagtgtgg agacaagact 3840
ggcaatcgtg gtcctttgca attcatggcg cgc (SEQ ID NO:2)

FIG. 5

Full length cDNA sequence of *CrcpSulP*: 1984 bp

```
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gtaagccacc agacactacc aagtagagta atccatttgt ataggtacag aatatggagc 180
gagtttgcag ccatcagctt gcctcgtcgc gagggaggcc atgcatcgct ggggtgcagc 240
ggtcgcccat ccgactaggg acttcaagcg ttgctcatgt gcaggtctct ccggcaggcc 300
ttgggagata tcaacggcaa agactgcaag tcgtggcgtc tgcagctgcg gcagcggctt 360
tcgaccctcc tggaggtgtc tccgccgggt tctcgcagcc gcaacagcag ctgccacaac 420
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caggtggtgg agggtgcagg gcggggtgtt gggatgggat gggatgggac cgtgggaggg 1560
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gggggaggca gggattgagc gaaggacgca ctgcaagctc aggcagtcgc atgcccgtac 1920
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(SEQ ID NO: 3)

FIG. 6

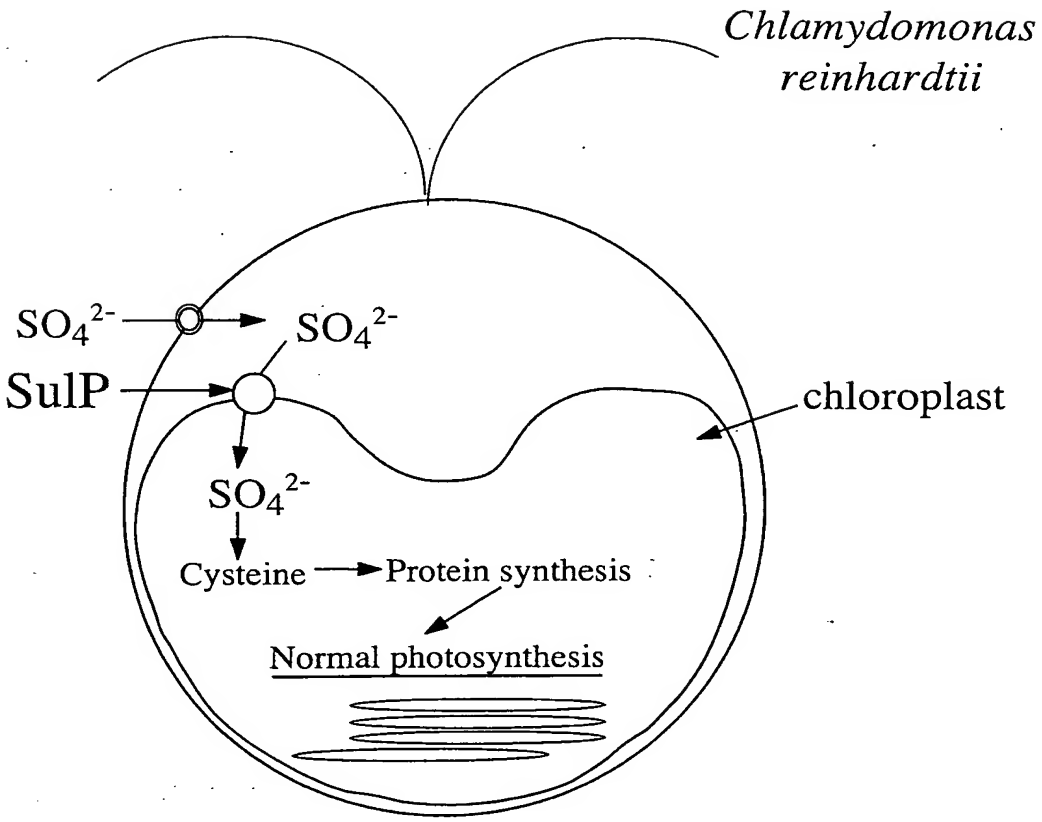
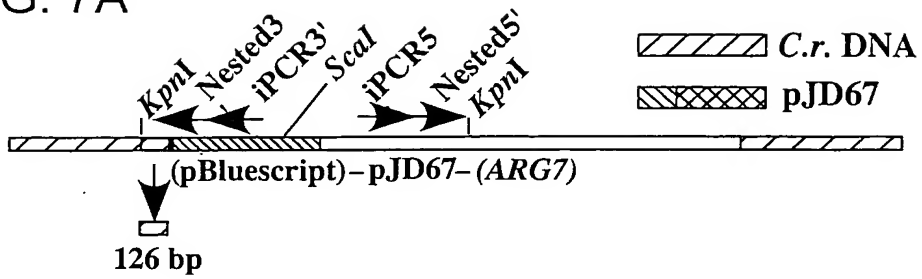

Chlamydomonas reinhardtii
SO_4^{2-}
SO_4^{2-}
SulP
chloroplast
SO_4^{2-}
Cysteine
Protein synthesis
Normal photosynthesis

FIG. 7A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Nested3'
iPCR3'
ScaI
iPCR5'
Nested5'
KpnI
C.r. DNA
pJD67
(pBluescript)–pJD67–(ARG7)
126 bp

FIG. 7B

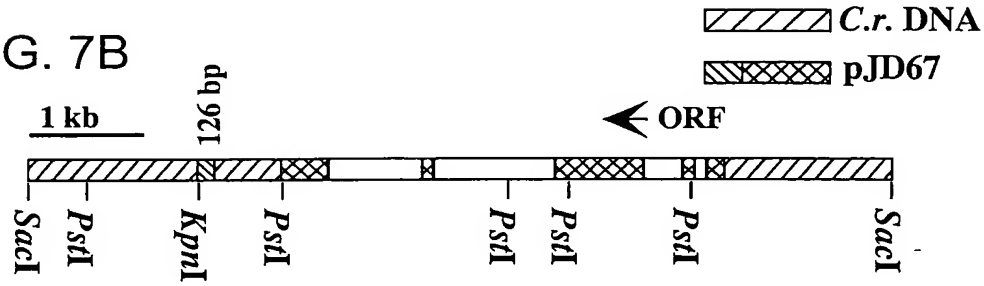
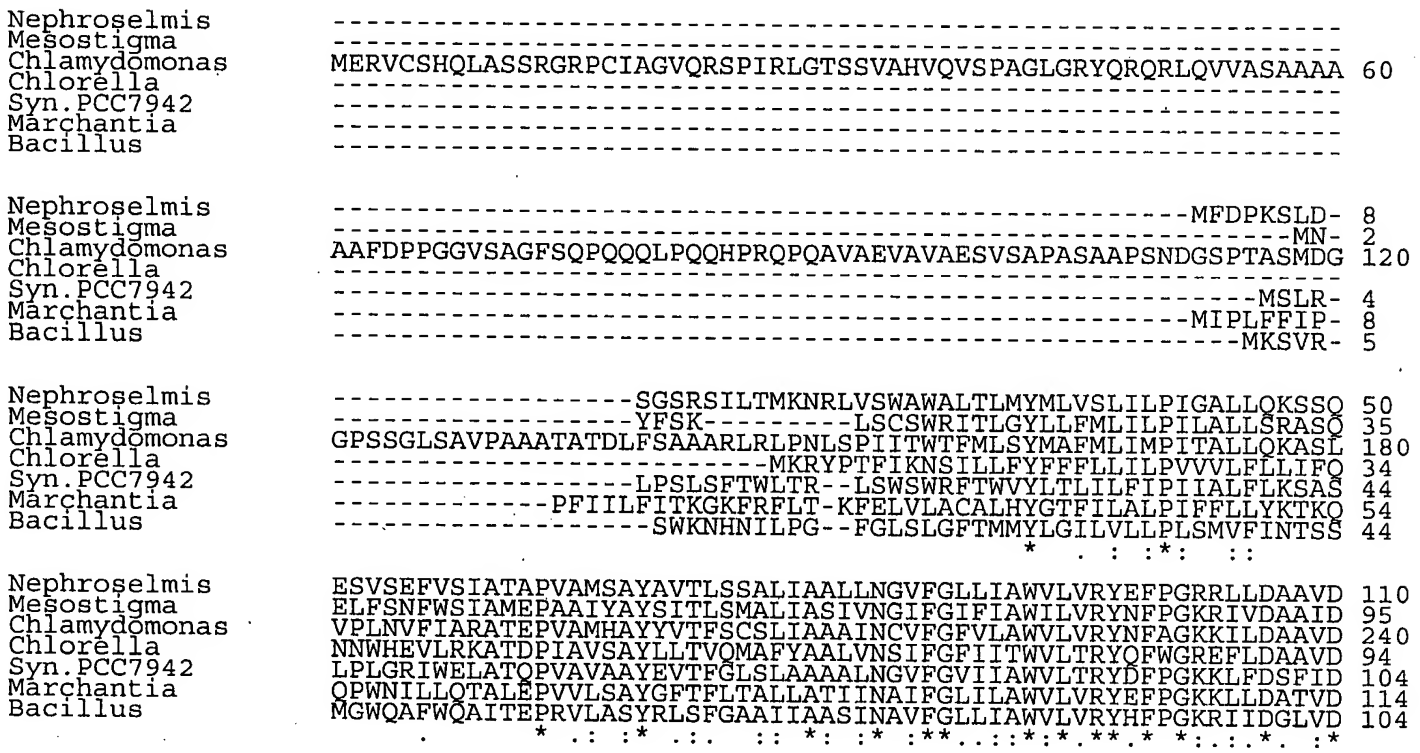

C.r. DNA
pJD67
1 kb
126 bp
ORF
SacI
PstI
KpnI
PstI
PstI
PstI
PstI
SacI

FIG. 8A


Nephroselmis
Mesostigma
Chlamydomonas
Chlorella
Syn.PCC7942
Marchantia
Bacillus
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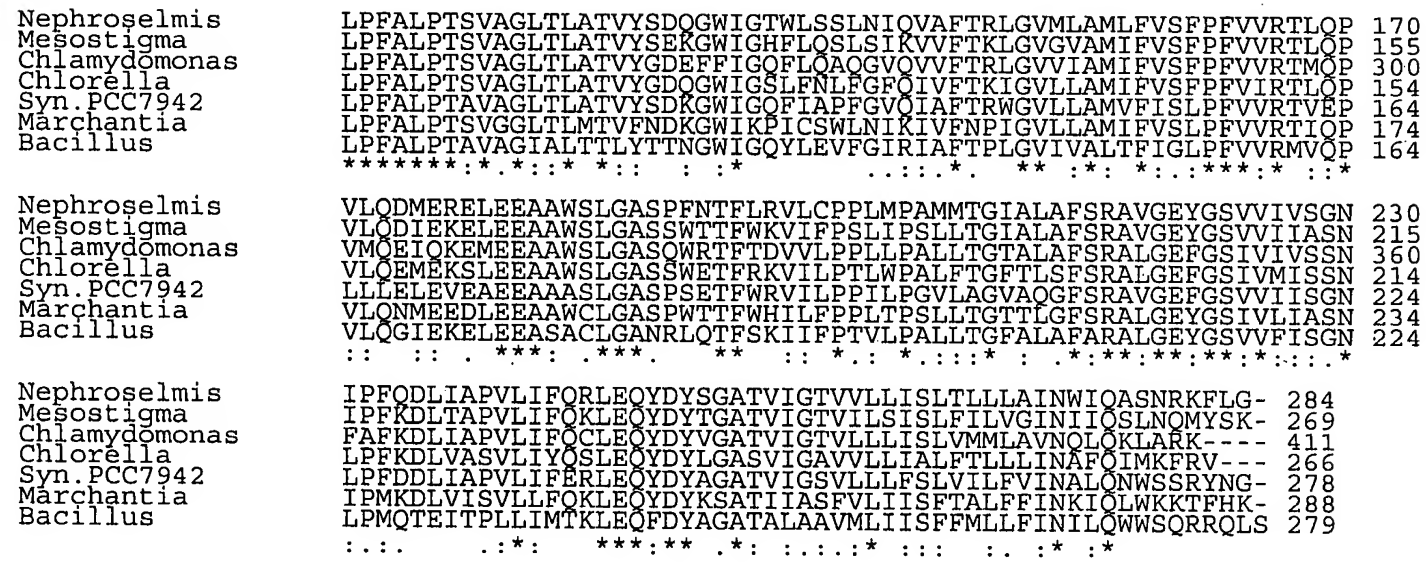
MFDPKSLD- 8
MN- 2
AAFDPPGGVSAGFSQPQQQLPQQHPRQPQAVAEVAVAESVSAPASAAPSNDGSPTASMDG 120
MSLR- 4
MIPLFFIP- 8
MKSVR- 5
SGSRSILTMKNRLVSWAWALTLMYMLVSLILPIGALLQKSSQ 50
YFSK---------LSCSWRITLGYLLFMLILPILALLSRASQ 35
GPSSGLSAVPAAATATDLFSAAARLRLPNLSPIITWTFMLSYMAFMLIMPITALLQKASL 180
MKRYPTFIKNSILLFYFFFLLILPVVVLFLLIFQ 34
LPSLSFTWLTR--LSWSWRFTWVYLTLILFIPIIALFLKSAS 44
PFIILFITKGKFRFLT-KFELVLACALHYGTFILALPIFFLLYKTKQ 54
SWKNHNILPG--FGLSLGFTMMYLGILVLLPLSMVFINTSS 44
ESVSEFVSIATAPVAMSAYAVTLSSALIAALLNGVFGLLIAWVLVRYEFPGRRLLDAAVD 110
ELFSNFWSIAMEPAAIYAYSITLSMALIASIVNGIFGIFIAWILVRYNFPGKRIVDAAID 95
VPLNVFIARATEPVAMHAYYVTFSCSLIAAAINCVFGFVLAWVLVRYNFAGKKILDAAVD 240
NNWHEVLRKATDPIAVSAYLLTVQMAFYAALVNSIFGFIITWVLTRYQFWGREFLDAAVD 94
LPLGRIWELATQPVAVAAYEVTFGLSLAAAALNGVFGVIIAWVLTRYDFPGKKLFDSFID 104
QPWNILLQTALEPVVLSAYGFTFLTALLATIINAIFGLILAWVLVRYEFPGKKLLDATVD 114
MGWQAFWQAITEPRVLASYRLSFGAAIIAASINAVFGLLIAWVLVRYHFPGKRIIDGLVD 104

FIG. 8A
CONT.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Mesostigma LPFALPTSVAGLTLATVYSEKGWIGHFLQSLSIKVVFTKLGVGVAMIFVSFPFVVRTLQP 155
Chlamydomonas LPFALPTSVAGLTLATVYGDEFFIGQFLQAQGVQVVFTRLGVVIAMIFVSFPFVVRTMQP 300
Chlorella LPFALPTSVAGLTLATVYGDQGWIGSLFNLFGFQIVFTKIGVLLAMIFVSFPFVIRTLQP 154
Syn.PCC7942 LPFALPTAVAGLTLATVYSDKGWIGQFIAPFGVQIAFTRWGVLLAMVFISLPFVVRTVEP 164
Marchantia LPFALPTSVGGLTLMTVFNDKGWIKPICSWLNIKIVFNPIGVLLAMIFVSLPFVVRTIQP 174
Bacillus LPFALPTAVAGIALTTLYTTNGWIGQYLEVFGIRIAFTPLGVIVALTFIGLPFVVRMVQP 164
Nephroselmis VLQDMERELEEAAWSLGASPFNTFLRVLCPPLMPAMMTGIALAFSRAVGEYGSVVIVSGN 230
Mesostigma VLQDIEKELEEAAWSLGASSWTTFWKVIFPSLIPSLLTGIALAFSRAVGEYGSVVIIASN 215
Chlamydomonas VMQEIQKEMEEAAWSLGASQWRTFTDVVLPPLLPALLTGTALAFSRALGEFGSIVIVSSN 360
Chlorella VLQEMEKSLEEAAWSLGASSWETFRKVILPTLWPALFTGFTLSFSRALGEFGSIVMISSN 214
Syn.PCC7942 LLLELEVEAEEAAASLGASPSETFWRVILPPILPGVLAGVAQGFSRAVGEFGSVVIISGN 224
Marchantia VLQNMEEDLEEAAWCLGASPWTTFWHILFPPLTPSLLTGTTLGFSRALGEYGSIVLIASN 234
Bacillus VLQGIEKELEEASACLGANRLQTFSKIIFPTVLPALLTGFALAFARALGEYGSVVFISGN 224
Nephroselmis IPFQDLIAPVLIFQRLEQYDYSGATVIGTVVLLISLTLLLAINWIQASNRKFLG- 284
Mesostigma IPFKDLTAPVLIFQKLEQYDYTGATVIGTVILSISLFILVGINIIQSLNQMYSK- 269
Chlamydomonas FAFKDLIAPVLIFQCLEQYDYVGATVIGTVLLLISLVMMLAVNQLQKLARK---- 411
Chlorella LPFKDLVASVLIYQSLEQYDYLGASVIGAVVLLIALFTLLLINAFQIMKFRV--- 266
Syn.PCC7942 LPFDDLIAPVLIFERLEQYDYAGATVIGSVLLLFSLVILFVINALQNWSSRYNG- 278
Marchantia IPMKDLVISVLLFQKLEQYDYKSATIIASFVLIISFTALFFINKIQLWKKTFHK- 288
Bacillus LPMQTEITPLLIMTKLEQFDYAGATALAAVMLIISFFMLLFINILQWWSQRRQLS 279

FIG. 8B

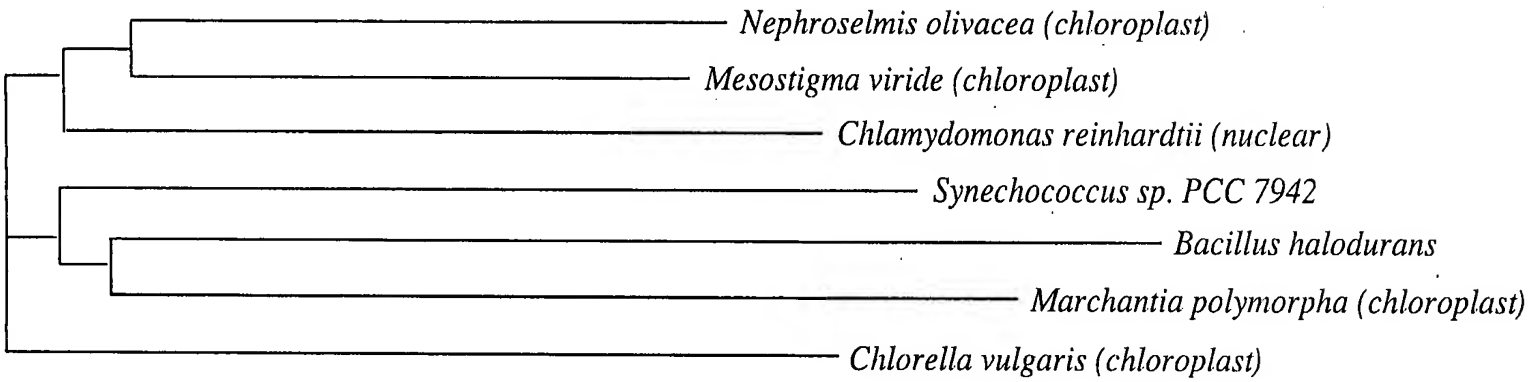

Nephroselmis olivacea (chloroplast)
Mesostigma viride (chloroplast)
Chlamydomonas reinhardtii (nuclear)
Synechococcus sp. PCC 7942
Bacillus halodurans
Marchantia polymorpha (chloroplast)
Chlorella vulgaris (chloroplast)

FIG. 9

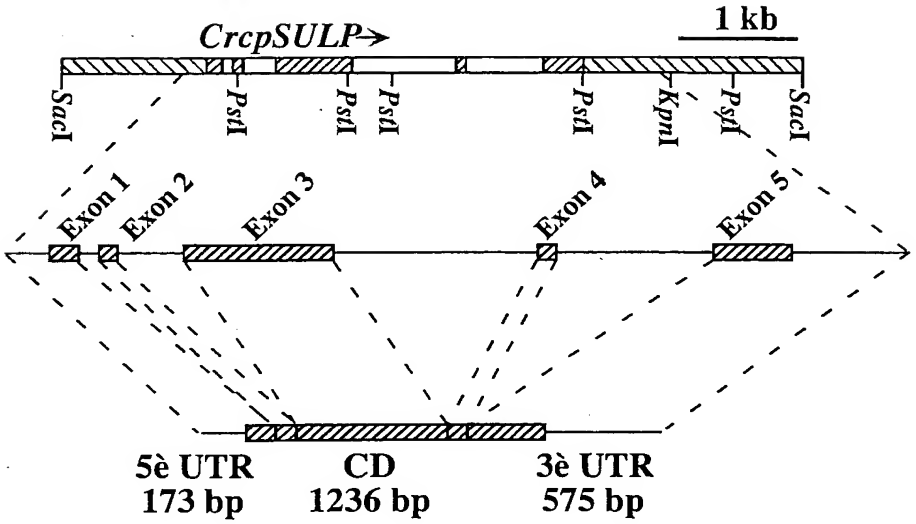
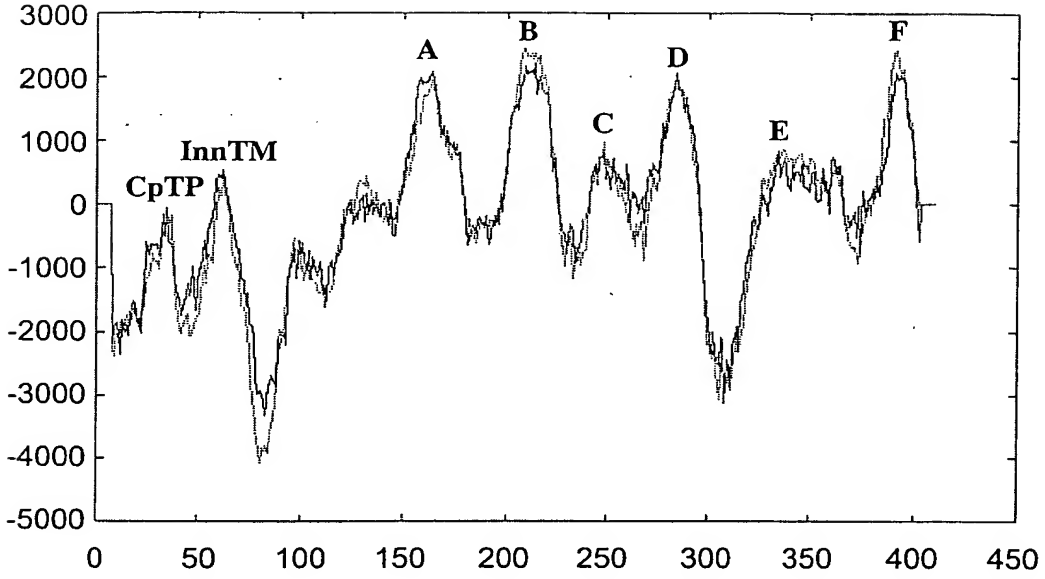

CrcpSULP
1 kb
SacI
PstI
PstI
PstI
PstI
KpnI
PstI
SacI
Exon 1
Exon 2
Exon 3
Exon 4
Exon 5
5è UTR
173 bp
CD
1236 bp
3è UTR
575 bp

FIG. 10


3000
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1000
0
-1000
-2000
-3000
-4000
-5000
0
50
100
150
200
250
300
350
400
450
A
B
C
D
E
F
InnTM
CpTP

FIG. 11A

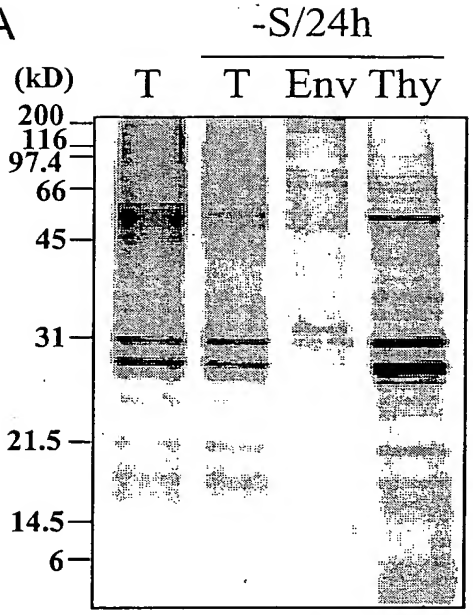


FIG. 11B

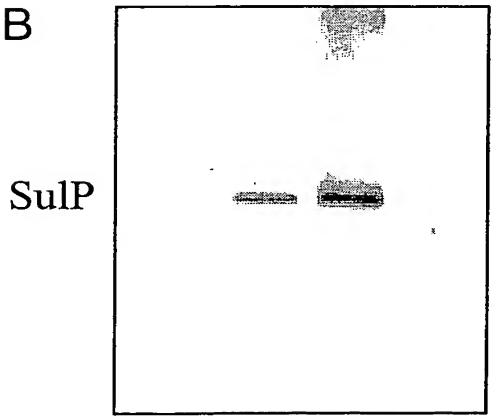


FIG. 12A

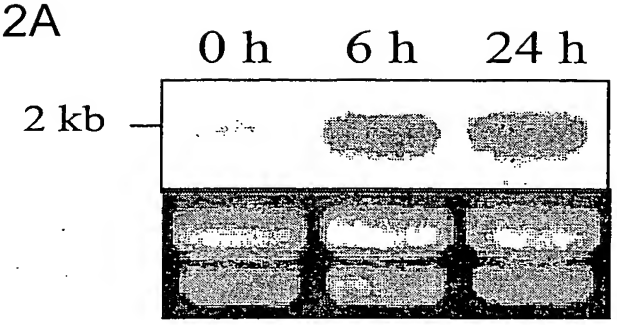


FIG. 12B

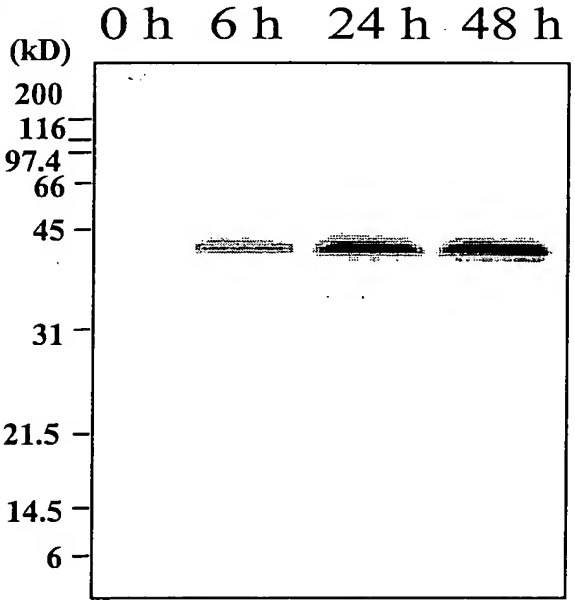
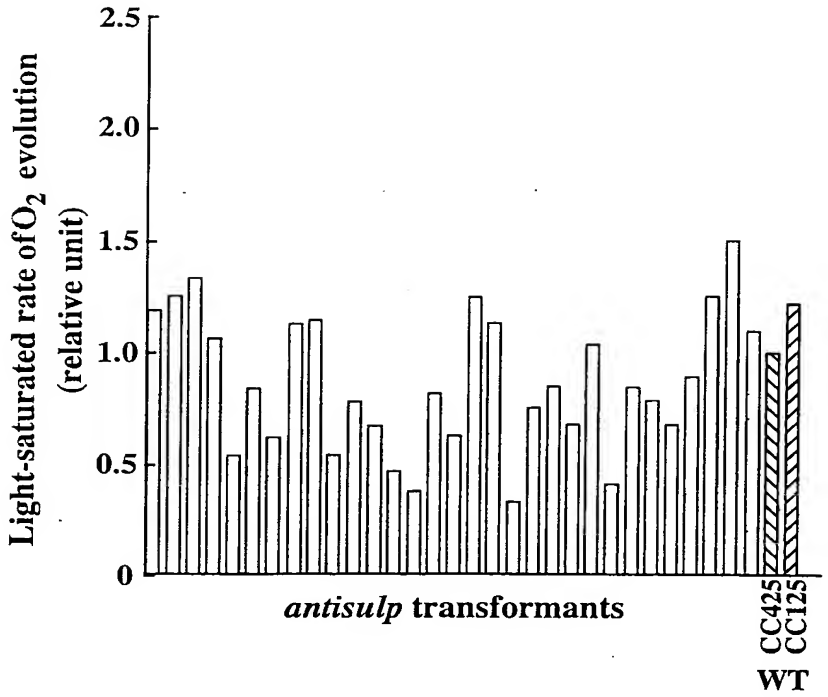


FIG. 13


Light-saturated rate of O_2 evolution (relative unit)
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2.0
1.5
1.0
0.5
0
antisulp transformants
CC425
CC125
WT

FIG. 14A

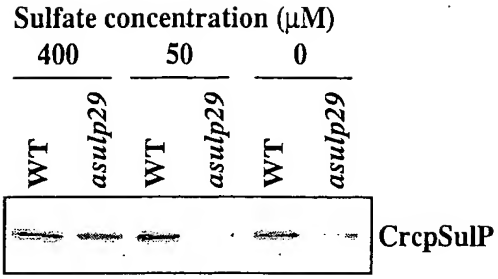


FIG. 14B

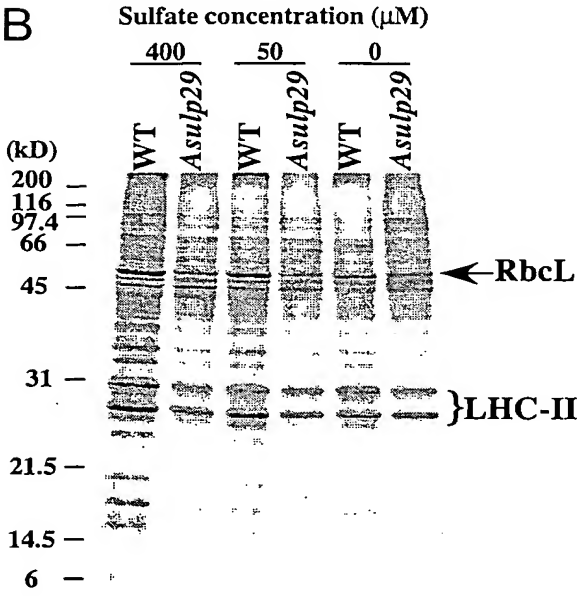


FIG. 14C

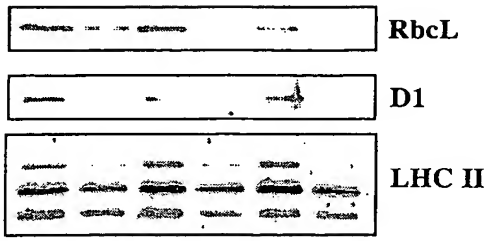


FIG. 15A

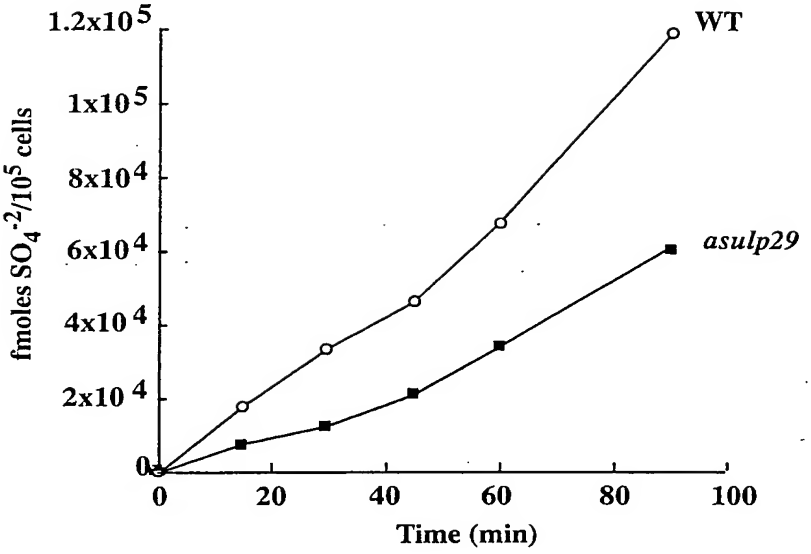
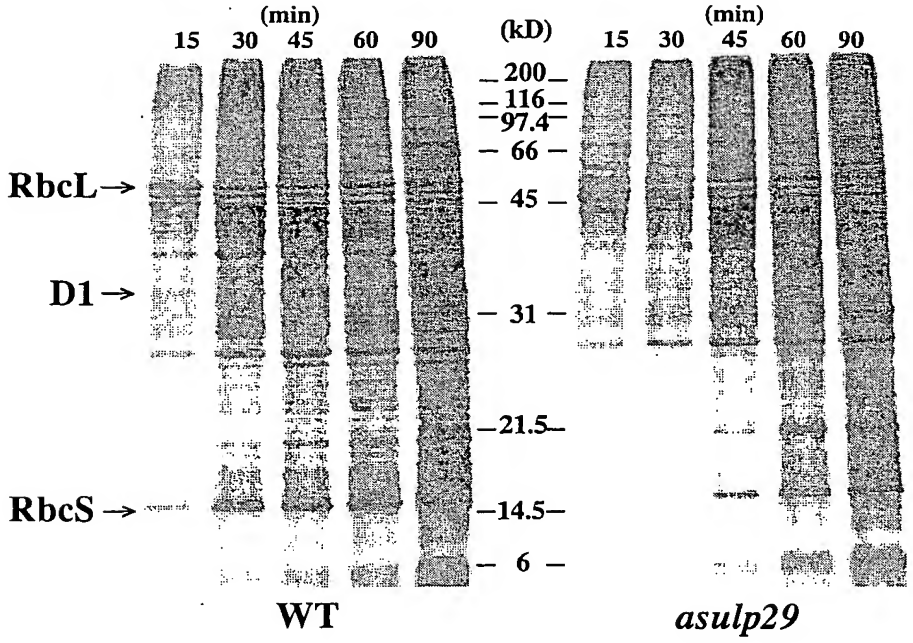
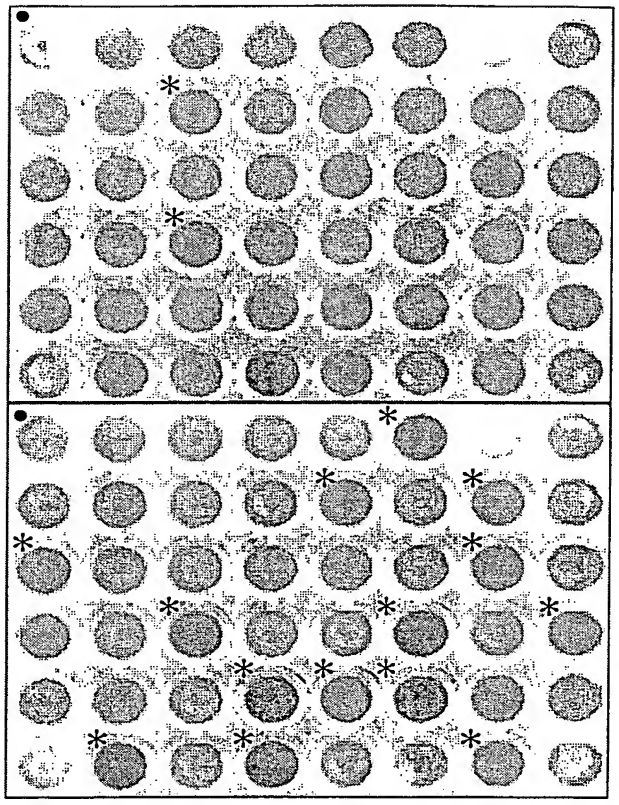


FIG. 15B



400 μM S
(TAP, S_{400})



150 μM S
(TAP, S_{150})

FIG. 16

FIG. 17

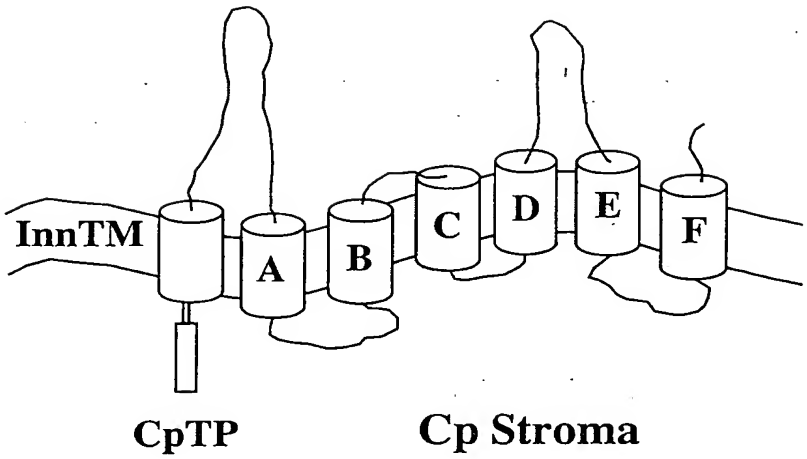


FIG. 18A

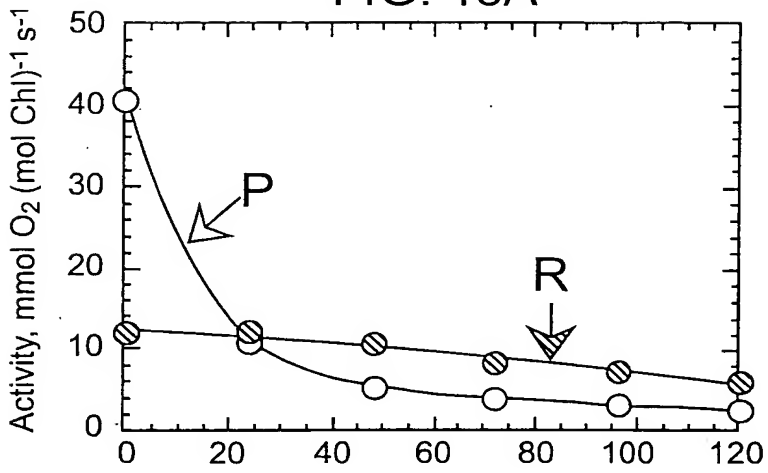


FIG. 18B

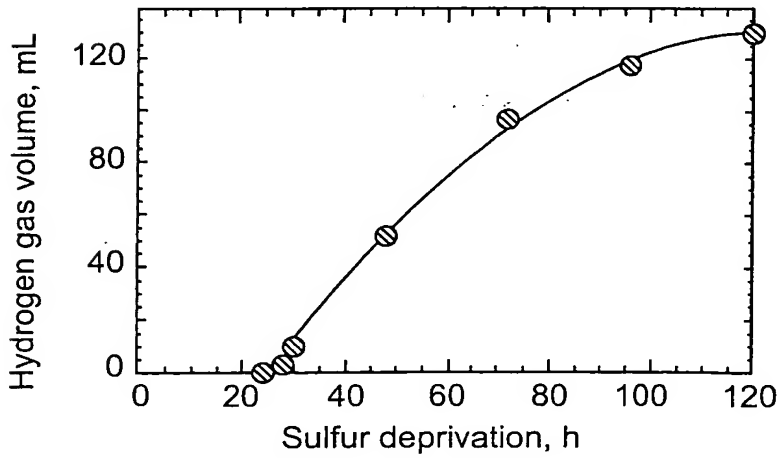


FIG. 19

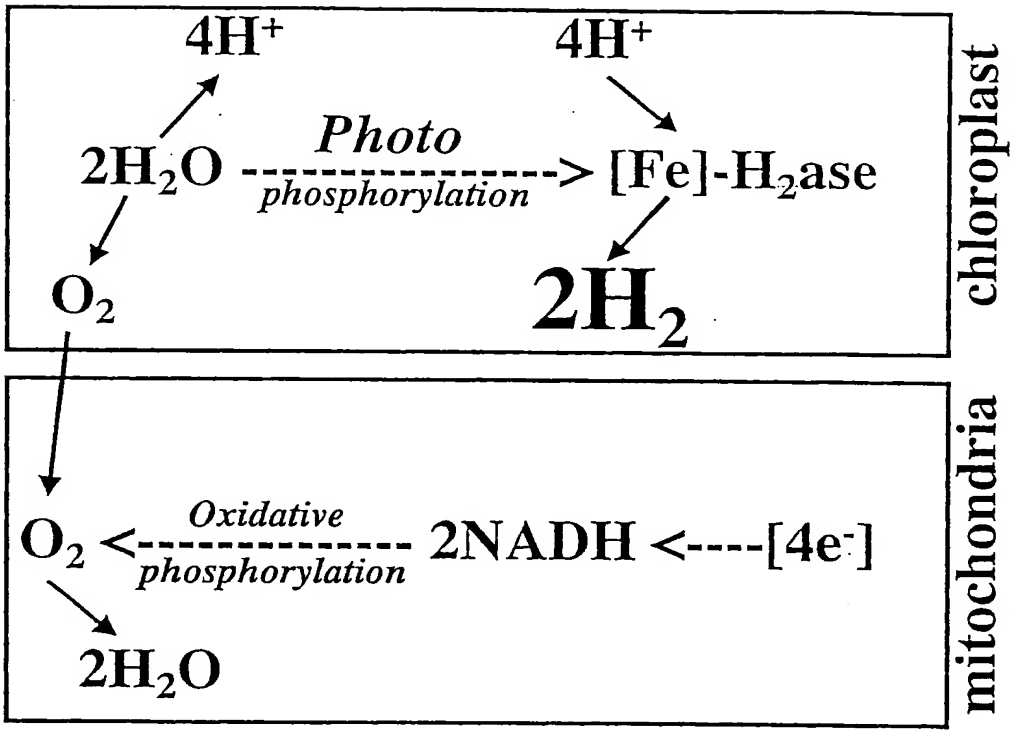
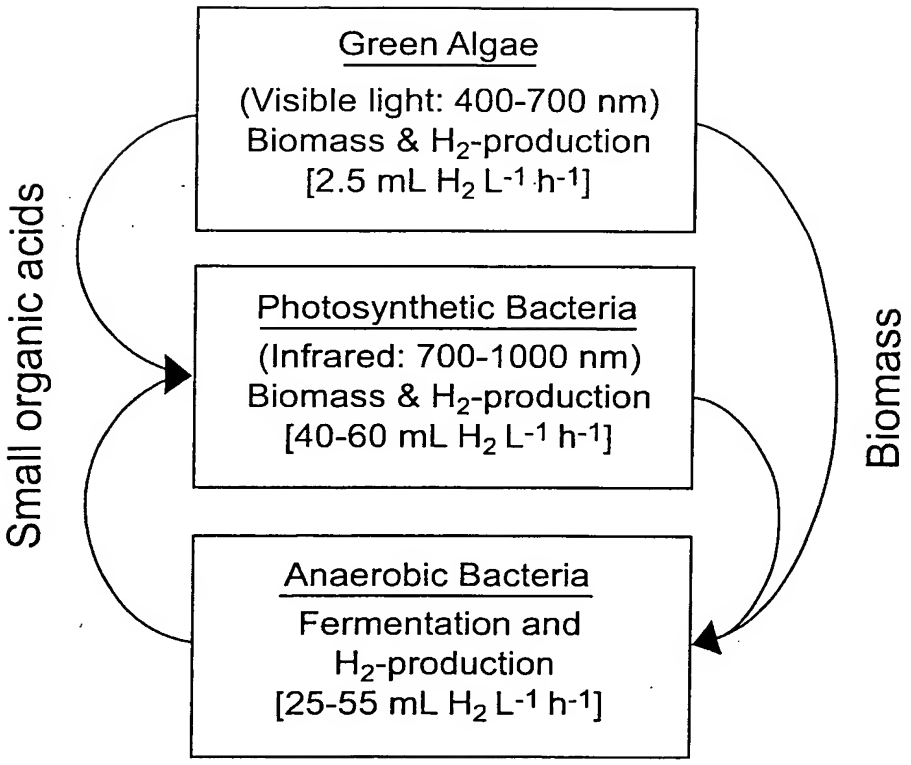

4H+
4H+
2H2O
Photo
phosphorylation
[Fe]-H2ase
O2
2H2
chloroplast
O2
Oxidative
phosphorylation
2NADH
[4e-]
2H2O
mitochondria

FIG. 20


Green Algae
(Visible light: 400-700 nm)
Biomass & H_2-production
[2.5 mL H_2 L^{-1} h^{-1}]
Photosynthetic Bacteria
(Infrared: 700-1000 nm)
Biomass & H_2-production
[40-60 mL H_2 L^{-1} h^{-1}]
Anaerobic Bacteria
Fermentation and
H_2-production
[25-55 mL H_2 L^{-1} h^{-1}]
Small organic acids
Biomass

CATTCAATTTGCAGCGTTCCTAAAATGGCAAGCACAACGCTGCTCCAGCCCGCGCTTGGTCTGCCCTCGCGGGTAGGG
CCTCGCTCCCCTCTGTCGCTTCCCAAAATTCCTCGCGTGTGCACGCACACTAGTGCTCCCTCTACCTCAAAGTACTGC
GACTCATCATCAGTTATAGAGAGCACGCTAGGGCGGCAAACATCGGTTGCCGGGAGACCATGGCTTGCACCCCGGCCT
GCGCCTCAACAAAGCCGAGGCGACCTACTGGTCTCCAAATCGGGGGCAGCAGGAGGCATGGGCGCCCATGGAGGGGGC
TTAGGGGAACCGGTCGATAATTGGATCAAGAAGCTACTCGTTGGTGTCGCGGCGGCGTACATCGGCTTGGTCGTGCTG
GTGCCCTTCCTGAATGTCTTCGTCCAGGCGTTCGCCAAGGGCATCATTCCCTTCCTGGAGCACTGCGCGGACCCGGAC
TTTCTGCACGCACTCAAGATGACGCTGATGCTGGCGTTCGTGACGGTGCCGCTCAACACGGTGTTTGGCACGGTGGCC
GCGATCAACCTCACGCGCAACGAGTTCCCCGGCAAGGTGTTCCTGATGTCGCTGCTGGACCTGCCCTTCTCCATCTCG
CCCGTGGTGACTGGCCTGATGCTCACGCTGCTGTACGGCCGCACCGGCTGGTTCGCGGCGCTGCTGCGGGAGACCGGC
ATCAACGTGGTGTTCGCATTCACGGGCATGGCCCTGGCCACCATGTTTGTGACGCTGCCGTTCGTGGTGCGCGAGCTG
ATCCCCATCCTGGAGAACATGGACCTGTCGCAGGAGGAGGCGGCGAGAACGCTGGGGGCCAACGACTGGCAGGTGTTC
TGGAACGTGACGCTGCCCAACATCCGCTGGGGCCTGCTGTACGGCGTGATCCTGTGCAACGCCCGAGCCATGGGCGAG
TTCGGAGCCGTGTCCGTCATCTCGGGCAACATCATCGGCCGCACGCAGACGCTGACGCTGTTCGTCGAGTCCGCCTAC
AAGGAGTACAACACGGAGGCGGCGTTCGCGGCGGCTGTGCTGCTGAGCGCGCTGGCGCTGGGCACCCTGTGGATCAAG
GACAAGGTGGAGGAGGCGGCGGCGGCGGAGAGCCGCAAGTAGAGAGGAGCAGGCGGCGTCGGCAGCGGCGGCAGTGGC
AGCGGCAGCGGCGGAGAGCGGCAGCTGGAGAGGAGCAGGCGGTGGCGGCGGAGCGGCGGAAATAGAGAGGTGCAGCAA
GGAGGCAGGCGCCGACGCGAGGGGAGGGCGTGGTGGTGGGCTTGCGTGGGTGCTTGGTCCGTGGCCAGGGTGCCTGGC
CTGGGTAGTTGGTGTGTGGGTGAAGCTGATTCCTGTTTGGGTGAGGCGGCCGAGTTCCTGAAGGAAGCAAGGAAGGAC
AGTGCCGCAGTGACCAGCGGGTAATGGTAAGGGAGCTGACACGTGTGGCGTTCTGTTGCTGGTCGCCGCATGCTTAAC
GCAGCGGGAGCAGCTTCTCTGTCTGATGTCTAACGGGGGCGTTGTATGCTGATAATAGACGGAGGGCGAAGGGAGCAG
GCGCGGTTCAGATGGGGTAAAAGCTGTTGGAAATCAACACGTGCAGCGGGTGGGTTGCATTTGTGATCACTGGACGTT
CTGAGTGGTCCGTGCGCCTATAGCGCGTGCTGTGCATATATACGCGCGCCGGCGCATAAAACATGACTGCATGTGTCG
GTGTTGACGGTACAGTTATGCCGTGCCCCGTTTTACAAGCGGGATAGAGGCACACTCCACGTAGTATGCATTGAGCCC
AGTAGACTCTGGTCAGAAGGCCGGTAAATTTACATGTGTCGTGGTGAACCCTGTAAGTCATGGCCCAAG
(SEQ ID NO: 04)

FIG. 21

GTACTTCAATTGTCAGAATGGCGTCGCTGCTCGCTCAAACAACATCGCGCCTTGGCGCTCGCCCAGCTGCGCAA
GCTGGCCCTGTCGCCCAAATGGCACCGATGGCAAGCCGAGTGCAGCCGGCGATGCCTAGCGCGCTGCTCCCACT
GCACGCCAGAGCGACAACAACTTCAGTCGCTTGCCGGGCAGCCAGCATCGACAAACCTGTCGTTTACACTCCTC
GAGATTCGTCGCAACAGTCCTCCAATGGGGCAGGAGAAGTGTCCATGTCCATATCATCCATGGACGAGGTTGGA
CCCTCTTATGAGGGAATCATTACAGACGCGCCTACACGACCAACGGGGCTTTATGTGCGGGTGCGCAACATGGT
GAAGCACTTCAGCACCGCCAAAGGCCTGTTCAGGGCGGTGGACGGCGTGGACGTGGACATCGAGCCCAGCTCCA
TCGTGGCGCTGCTGGGGCCCAGCGGCAGCGGCAAGACCACATTGCTGCGCCTCATTGCAGGCCTGGAGCAGCCC
ACGGGCGGCAACATCTACTTTGACGACACGGACGCGACCAACCTGTCCGTCCAGGACCGCCAGATCGGCTTCGT
GTTCCAGAGCTATGCGCTGTTCAACCACAAGACAGTTGCGGAGAACATCAAGTTTGGACTGGAGGTGCGCAAGC
TCAACATCGACCACGACAAGCGCGTGGCGGAGCTGCTGGCGCTGGTGCAGCTCACCGGCCTGGGCGACCGCTAC
CCGCGCCAACTGTCGGGCGGCCAGCGGCAGCGTGTGGCGCTGGCGCGCGCCCTGGCCTCCAACCCGCGGCTGCT
GCTGCTGGACGAGCCCTTTGGCGCGCTGGACGCGGTGGTGCGCAAGCAGCTGCGCACGGGGCTGCGCGAGATCG
TGCGCAGCGTGGGCGTGACCACCATCATTGTGACGCACGACCAGGAGGAGGCGTTCGACCTGGCGGACAAGGTG
GTGGTGTTCAACAGGGGCCTGGTGGAGCAGCAGGGCAGCCCCACCGAGATCATCAAGCGGCCGCGCACGCCCTT
CATTATGAAGTTCGTGGGCGAGACCAACGTGGTGCCGGCCACGTCGCTGCTGGCCAAGCGCATGCGCTTCAACA
CCTCCAAGACCAGCGTCATGTTCCGGCCGCACGACATTAAGCTGTTCAAGACGGTGCCGCCGGAGAGCGGCGAG
GGCGCGCTGACCACGGTGGGCGCCAACGTGGCGGACAAAGCCAACCTGGGCTGGGTGGTCAAGTACACGCTGCG
CTTCGATGACGACGTGGAGTGCGAGCTGCAGCTCAGCCGCGACCAGGACGAGCGCGAGTACAACCTGGTGGTGG
GCAGCCGCGTGTTCGTGCACGTGCCGCACCGCACCATGATGGGCTTCAACGCCAGCGACGTGGACAGCACGCCC
ATCGTGTAATGTGCGGGGTTGGCGGCTGTGGCCAGCGATTGTTGCAATGCAGTCCAGCGTGCTCTTGGTTTGGT
TCCAGTGACACCCATCCAGGGCACAGGTCCCTGAGCAGCGGGTGTTGGTGATGGGTTGGAGCAGTTGTACCCGA
TTCTCGCATGCAAGGGGGCGGGGCGCCCACGGGGTGGGAGAGCGGAATGGCGGTGAGGTGGGCTACTGCATGCG
GCCGTGGAGGAACGGAGGGGTGCACAGGCGGGCAGGTAGACAGGCGGAGCGGGCTGGGTGAGCGGGGCTGTAGT
TTGGGGGTGGAGGCCGTGCAGACTGGTTGGGATACTGACAGATCAATGAGCGGCGTCTGCTCCATGGGTCAGTA
GGAGAGCGGTGTGGGTGTGTGCAGTTGCGAGTTCTGGAGCGTTGTGCGCCTCGCGCTGTGTGCGCGCGCCCGTG
CGTCTGCGGGCGCTGTCGGAGACGGGCGATGTACATGAAGCTGGACCTGGGCCTGTCTCACAAATATCCCTTAT
GTTAATAGTAGGATGTCGCAATCGTGCCTTGGAGCCCACCTGATGTGTGTGTCACAGGTGGCAGTAGTTTGGCC
TTGCGGGAGGTAGCACGTCTTTCATGAGAGTGCGTGTGCGTGACCGCTTTTACATTGCCAATCACGCTGGAAGG
TGAAACCATGCATCATGCGTGCTATCAGGAGATGCAGACGGCGGATTGCTGCCAAAATGTTCTGTTGTTGGTGT
GCAGACTTGGTGGCGAAGGGGCCAGGCGCCCAGGGGTATGCTGCGTGCCAAGGAGCTGCTGCCGCCACGAGTGA
CCAGCGAAACTTGTAAATTGAATATTGTATCCT (SEQ ID NO: 05)

FIG. 22

GGGCAGCGTATAAGTAATGTCGTTCTTGGCTCCCAGCTTAGGCGTCGCGCGGGGGATTCTGGAGCCGGCGAGTGC
AGCGAGGCCGCCTGCGCACGCGGCCGGTCACGCACCCGTTCTAACAAGCGATAGGACTGGTGGACCTGCCGCTAA
TCATGACAGGCCTGCCGGTGCTCCCAGCCCCCATGCGGCGTCGTTGACGCCCTCCAGCAGCGGGCAAGCAAGCCA
GCAAGGCGACCCCCAGCGCTCGCAGCACCAGCAAGCGCAGCGCCAGGACCAGCAGCAGTCGCAGTCGCGGTCGCT
CCAATCACACCTCATCACCGCGGCCACGCTGCTGCCAGCCCTGCCGCCTCCGCCTCCCGGCGGCAACGGCGACGG
CGATGGCGGCGAAGCTGCGGGGCCGCAGCCGCTCGCGGACGTCGCGGCTCAGCCGCCGGAGGTTGTGCTGACGCT
GGCGTCGTTCGCGGTGACCAAGCTGGCGTACGTGCGTGTGACGCGCGCGTTCCGGGAGTGGTACGAGCGCACGAA
GGGCGTGGATGTGCGCTTCCGCCTCACCTTCGCCGCCAGTGGCGTGCAGGCCCGCGCCGTGATCGATGGCCTGCC
CGCCGACATCGTGGCCCTGGCGCTGCCTCTGGACCTGGACAAGATCGTGTCGGCGGGGCTGATCCGGCCCGACTG
GCGCAGCGCCTACCCGGCAGCCAGCGTGGTGTGCGAGACCACCGTGGCGTTCGTGGTGCGCCAGGGCAACCCCAA
GAACATCCGCACCTGGGAGGACCTCACGCGGGCGGGTGTGGAGGTGGTGCTGGCCAACCCCAAGACCGCCGGAGT
GGCCAGGTGGATCTTCCTGGCCCTGTGGGGCGCCAAGATGAAGAAGGGCAACGCCGCCGCGCTGGCGTATGTGCA
GCGCGTGTTCGAGAACGTGGTGGTGCAGCCGCGTGATGCGCGCGAGGCGTCGGACGTGTTCTATAAGCAGAAGGT
GGGCGACGTGCTGTTGACGTACGAGAACGAGGTGATCCTGACCAACGAGGTGTACGGCGACAAGGCGCTGCCGTA
CCTGGTGCCCTCCTACAACATCCGCATCGAGTGCCCGCTGGCGCTGGTGGACAAGGTGGTGGATGCCCGCGGCCC
CGAGGTGCGCGAGGCGGCGTCCGAGTTCTGCCGTTTCCTGTTCACGCCCGCGGCGCAGCACGAGTTCGCGCGGCT
GGGCTTCCGCGTGAACCCGCGCACCTGCAAGGAGGTGGCGGCGCAGCAGACCGGACTGCCGCCCGCAAACCTGTG
GCAGGTGGACAAGGAGCTGGGCGGCTGGGCTGCGGCCCAGAAGAAGTTTTTCGACGCTGGCGCCATCCTTGACGA
CATCCAGTCCGCCGTGGGCAAGCTGCGTGTGGAGCAGCGCAAGGCGGCGCAGGCGGCGGCCAGGCGGTAGAGAGA
CGCGGTACAAGTGCTCGGGTGCTCAGCAGGAGCTGCAGCAGGGGCAGCAAGAGGGCCTTGACAGGAGGGAATGGT
AGGCAAAGGCGGCAGGGGAGGCGGGATGGCGGGATGAAGTGAGGGTGTGCAAGCAGCGATGTGTGCCAAGGACGG
TGTCGGCGATGTACATGATAACATGAGGAGACAGGAGCATCTCCTGGCAGGAGGCGGCAACCGTGGAGTGTCTGA
AAGGAGAACTTGATTGCTCAGTGTGGGACAGATAACGGAGGGCGGGGTGTGGGGCGTGGGGCTTATCGGTGTGCT
TCTATGGGGAGGCCTGACTGCATTGGGGGCGACGTAGTGTGATGGCCGCTACACGCTTGCTCGGAACTGACATAA
ACAGGCGTTCAGGCCATGGCTGCATGAGGCTTGATGTCGTATCGCGGACTGTC (SEQ ID NO: 06)

FIG. 23

MASTTLLQPALGLPSRVGPRSPLSLPKIPRVCTHTSAPSTSKYCDSSSVIESTLGRQTSV
AGRPWLAPRPAPQQSRGDLLVSKSGAAGGMGAHGGGLGEPVDNWIKKLLVGVAAAYIGLV
VLVPFLNVFVQAFAKGIIPFLEHCADPDFLHALKMTLMLAFVTVPLNTVFGTVAAINLTR
NEFPGKVFLMSLLDLPFSISPVVTGLMLTLLYGRTGWFAALLRETGINVVFAFTGMALAT
MFVTLPFVVRELIPILENMDLSQEEAARTLGANDWQVFWNVTLPNIRWGLLYGVILCNAR
AMGEFGAVSVISGNIIGRTQTLTLFVESAYKEYNTEAAFAAAVLLSALALGTLWIKDKVE
EAAAAESRK* (SEQ ID NO: 07)

FIG. 24

MASLLAQTTSRLGARPAAQAGPVAQMAPMASRVQPAMPSALLPLHARATTTSVAC
RAASIDKPVVYTPRDSSQQSSNGAGEVSMSISSMDEVGPSYEGIITDAPTRPTGL
YVRVRNMVKHFSTAKGLFRAVDGVDVDIEPSSIVALLGPSGSGKTTLLRLIAGLE
QPTGGNIYFDDTDATNLSVQDRQIGFVFQSYALFNHKTVAENIKFGLEVRKLNID
HDKRVAELLALVQLTGLGDRYPRQLSGGQRQRVALARALASNPRLLLLDEPFGAL
DAVVRKQLRTGLREIVRSVGVTTIIVTHDQEEAFDLADKVVVFNRGLVEQQGSPT
EIIKRPRTPFIMKFVGETNVVPATSLLAKRMRFNTSKTSVMFRPHDIKLFKTVPP
ESGEGALTTVGANVADKANLGWVVKYTLRFDDDVECELQLSRDQDEREYNLVXGS
RVFVHVPHRTMMGFNASDVDSTPIV* (SEQ ID NO: 08)

FIG. 25

MSFLAPSLGVARGILEPASAARPPAHAAGHAPVLTSDRTGGPAANHDRPAGAPSPH
AASLTPSSSGQASQQGDPQRSQHQQAQRQDQQQSQSRSLQSHLITAATLLPALPPPP
PGGNGDGDGGEAAGPQPLADVAAQPPEVVLTLASFAVTKLAYVRVTRAFREWYE
RTKGVDVRFRLTFAASGVQARAVIDGLPADIVALALPLDLDKIVSAGLIRPDWRSA
YPAASVVCETTVAFVVRQGNPKNIRTWEDLTRAGVEVVLANPKTAGVARWIFLAL
WGAKMKKGNAAALAYVQRVFENVVVQPRDAREASDVFYKQKVGDVLLTYENEV
ILTNEVYGDKALPYLVPSYNIRIECPLALVDKVVDARGPEVREAASEFCRFLFTPAA
QHEFARLGFRVNPRTCKEVAAQQTGLPPANLWQVDKELGGWAAAQKKFFDAGAI
LDDIQSAVGKLRVEQRKAAQAAARR* (SEQ ID NO: 09)

FIG. 26

FIG. 27

Chloroplast Sulfate Transport System